

A; Reference number: A89758; MUID:21311952; PMID:11418146
 A; Accession: C89921
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-3890 <KUR>
 A; Cross-references: UNIPROT:O99U53; GB:BA000018; PID:913701233; PID:BA842528.1; GSPDB:Q
 A; Experimental source: strain N315
 C; Genetics:
 A; Gene: ebbB

Query Match 6.7%; Score 98; DB 2; Length 3890;
 Best Local Similarity 22.3%; Pred. No. 49;
 Matches 65; Conservative 48; Mismatches 114; Indels 64; Gaps 14;

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Qy 3 YKCLLVRSLALISLMSILPQ---SPADPGSRTNDNKEFYISAKYNPSISHPRKFASEB 59
Db 892 YNKV-VASNMNSNAVILPDDIPPTINNPQ-----INNKY-----YRGDB 930
Qy 60 TPINGTNSTLTKVFGKKGKDITKKDDPFRVARGIDFONNLISPGSGTGYSMGPRIEL 119
Db 931 --VNPFTMGYSDRHSGIKNTNTITLPGWTSNLTKSDNKN-----GSAIT---GRVSM 978
Qy 120 EAAYQQ--FNPKNNDN-NDTDNGEYYKHFALSKDAMEDDQTYVVLKNDGIFTMSLWNT 175
Db 979 NQAFNSDITFVKSAATDYNNTNTDQSKEVSIHYGKISEDAHPVILGN---TEKVVVNP 1035
Qy 176 CYDITAEGTSFVPPVACAGGADLITIFKDLNLKFAYQKIGISYVITPVSAPIGGYHG 235
Db 1036 TAVSNDEKQS-----ITTAFKNKNQNI--RGYLASTDPVTNNNGVTLHYRD 1081
Qy 236 VIGNKPEKIPVIT--PVVNLND----APOTTSASVTLVGYFGGEIGKRF 279
Db 1082 GSSTTLDATNMTYBPPVKEYQTANAAATIATVIAKGSFNGDIKQFT 1132
  
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Search completed: February 17, 2005, 16:58:05
 Job time : 42 secs

A;Molecule type: mRNA	Qy	156	-----QQXYVVLKNDGKTFMSLMLVNTCYDITAEGVS--FVPYACAGIGADLITIPKD 204	
A;Residues: 1-69 <SIT>	Db	109	GIGGLKD1BDQTLKBERG-----	
A;Cross references: GB:M62972; NID:gi157263; PID:AAA28476_1; PID:gi157267			ARRSPFF1PYGTSNMSGVAI---	150
C;Genetics:				
A;Gene: DmRP140	Qy	205	LNLKPAYQKGKIGISYPITPEVSAFIGGYHGVIGNKEKI-----	PVITPV 250
A;Cross-references: FlyBase:FBgn0003276	Db	151	--KGWFKGP---NYCVT---SACATGNH--AIGDAFLQIKSDIDIA1AGGTEAATPL 199	
A;Introns: 8/1	Qy	251	-----VLNDAAFTTSAASVTLG--VGFQGSE 273	
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide	Db	200	GVAGPASMKALSTRNDEFOKAQRPFDRDGFVME 235	
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger				
Query Match 7.0% ; Score 102; DB 2; Length 1176;				
Best Local Similarity 19.9%; Pred. No 4.7;				
Matches 53; Conservative 39; Mismatches 78; Indels 96; Gaps 12;				
RESULT 14				
Qy 21 YQSPADPVSRTNDKKEGIVSFKRPSAETTPINSTSITKVGGLKKGD 80				
Db 813 YRSYKDSENKRVGQEENF-----BPKPHGTCQ-----GM-RNAH 846				
Qy 81 ITRKKDDFTTRVAGPQDFQNNLISGPGSISGYSMDGPRIELAAYQOFNPNTDNTDNGE 140				
Db 847 YDCLDUDG1TAIPI-----LBDNDDLSNTKR 888				
Qy 141 YYKH---PALSRKDAMEQQTQVVLKNDGITEMSLMV-----NTCY 177				
Db 889 PSKRDASTFLRNSETGIVQMLTINSEYKFCIRVSRVPIQIGDKFASRHGQKGTG- 947				
Qy 178 DITAEGVSP---FVYACAGIGADLIT-----IFKDNLNKF-AYQKGKIGISY 219				
Db 948 -----GIQRQEDMAFTCGEGLADIIINHAIPSRTMTGHLIBCQGKGSNKGIEDAT 1002				
Qy 220 PI-----TEVSAF1GGYTHVGIVNK 240				
Db 1003 PFENDAVNQVK1S1RPLQEQYXHLRNE 1028				
RESULT 13				
B70448 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus				
C;Species: Aquifex aeolicus	Qy	6	Query Match 6.8%; Score 100; DB 2; Length 1582;	
C;Accession: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004	Db	1	Best Local Similarity 21.4%; Pred. No. 10;	
R;Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On	Qy	2	Matches 63; Conservative 30; Mi matches 84; Indels 118; Gaps 13;	
Nature 392, 353-358, 1998	Db	3	39 FYTSAKNPNSISHFRKPSAETPINGNLSLTKEVGLKKGDDITKDDFTRVAPGIDFQN 98	
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.	Qy	4	548 FYMAGE---IGSFNFNGEST-----LDGALTVDSTPDNMPG---N 583	
A;Reference number: A73300; MUID:98196666; PMID:9537320	Db	5	99 NLISGGFCSI-----GYSMDGPPIELAYQQNPNTDNTDNGE 140	
A;Accession: B70448	Qy	6	584 DLJSNVGSTIKP1GQKEKPHVVKENAKSTATLQDSDDFDFTYVTF1KTPPEVIPSKEK 643	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	Db	7	141 YYKHFALSRKDAMED-----QQTYYVLLKNDG-----ITENSLMVN-----174	
A;Molecule type: DNA	Qy	8	644 VFETTRLSBAADEKTRMIGNDIMGSALKDYTPLADIGRITSPTKYMVNNINPSGV 703	
A;Residues: 1-415 <QFP>	Db	9	175 -----TCYDITASGVSPVYACAGIGADLITPKDNLKFAVQKIGSYPTPEVSAFI 229	
A;Cross references: UNIPROT:O67612; GB:AE000752; NID:92984021; PID:gi228	Qy	10	704 DTLSNSPFTDPLPKGLKMLEDIALNNS-----731	
A;Experimental source: strain VF5	Db	11	230 GGYGHGVIGNKFKP1VIT-----PVV-----INDAPOTTSASVTL-DYGG-YFG 271	
A;Gene: fabF		12	732 NKGHYYGFTNKFEGTPKFTNADQDVTIVYQKGHLYSKEVCIANTLNDYGVRTFG 786	
C;Function: fatty acid biosynthesis				
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein] synthase II				
C;Keywords: acyltransferase; fatty acid biosynthesis				
P;123-410/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>				
P;165/Active site: Cys #status predicted				
Query Match 6.9% ; Score 101.5; DB 2; Length 415;				
Best Local Similarity 21.7%; Pred. No. 1.3;				
Matches 60; Conservative 32; Mismatches 73; Indels 111; Gaps 14;				
RESULT 15				
C89921 hypothetical protein ebbh [imported] - <i>Staphylococcus aureus</i> (strain N315)				
C;Species: <i>Staphylococcus aureus</i>				
C;Accession: C89921				
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, Y.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiota, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirayatsu, K.				
Lancet 357, 1225-1240, 2001				
A;Title: Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> .				
Db 49 VKIAAEVKOFNPFEDMDKCEKARSKRFVQFAIAVKEALEDGSLLESEYDPYRVGVIIGT 108				

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OM protein - protein search, using sw model.
 Run on: February 17, 2005, 16:48:20 ; Search time 40 Seconds
 (without alignments)
 673.517 Million cell updates/sec

Title: US-10-680-349-42
 Perfect score: 1462
 Sequence: 1 MNYYKILVRLSALISLMSILP.....ASVTLDVGYFGGEIGMRFIF 280

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79.*
 1: pi1: *
 2: pi2: *
 3: pi3: *
 4: pi4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	629.5	43.1	276	2	JB0218	28k surface antigen
2	620	42.4	286	2	JB0219	28k surface antigen
3	603	41.2	280	2	JB0217	28k surface antigen
4	583	39.9	278	2	JB0216	28k surface antigen
5	565	38.6	284	2	I40882	major antigenic protein
6	515	35.3	287	2	I40920	28k surface antigen
7	386.5	26.4	282	2	I39648	major surface protein
8	227	15.6	133	2	I00221	28k surface antigen
9	119.5	8.2	264	2	I54665	heat resistant agg
10	107.5	7.4	239	2	AH0541	probable outer membrane protein
11	104.5	7.1	738	2	S01892	hemolysin A precursor
12	102	7.0	1176	2	A27826	DNA-directed RNA polymerase
13	101.5	6.9	415	2	B70448	3'-oxacyl-(lacyl- <i>ca</i> 3)-adhesin homolog
14	100	6.8	1582	2	AC1153	outer cell wall protein
15	98	6.7	3890	2	CB9921	peptidoglycan bound
16	97.5	6.7	274	2	AC3295	6-Phospho-Beta-D-Glucosidase
17	97.5	6.7	1174	2	S28976	endo-beta-N-acetylglucosaminidase
18	97.5	6.7	1271	2	A45555	hypothetical protein
19	97.5	6.7	1310	2	AD1380	hypothetical protein
20	95	6.5	1004	2	B25039	hypothetical protein
21	95	6.5	1578	2	AD1512	hypothetical protein
22	94.5	6.5	474	2	F97264	hypothetical protein
23	93.5	6.4	658	2	E95111	hypothetical protein
24	93	6.4	180	2	F1639	hypothetical protein
25	93	6.4	608	2	H64473	hypothetical protein
26	93	6.4	745	2	T51370	hypothetical protein
27	92.5	6.3	219	2	AF2658	conserved hypothetical protein
28	92.5	6.3	219	2	C97440	hypothetical protein
29	92.5	6.3	401	2	F86754	prophage pi2 protein

RESULT 2

JB0219	28k surface antigen 2 - Ehrlichia chaffensis
N;Alternate names: MAPI	C;Species: Ehrlichia chaffensis
C;Date: 21-Aug-1998 #Sequence_revision	C;Accession: JE0219
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.	A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe I
A;Reference number: JE0216; PMID:98321180; PMID:9647746	A;Molecule type: DNA
A;Residues: 1-276 <RED>	A;Cross-references: UNIPROT:Q93DD2; UNIPROT:Q9AC19; GB:AF062761
Query Match 43.1%; Score 629.5; DB 2; Length 276;	Best Local Similarity 47.9%; Pred. No. 8.3e-44;
Matches 137; Conservative 41; Mismatches 87; Indels 21; Gaps 6;	
Qy 1 MNYKKILVRLSALISLMSILPQSPADPVGSRNDNKEGYISAKYNPSTISHPRKPSAET 60	61 PINTGNTSLTKVTCGLKKQDG----ITCKDDPFRVAPGIDPQNSNDLISCFSGSGYSSAK 114
Db 1 MNYKKVFTISALISLSSLSPGVSESDPAGSGINGN--PYISGKYMPSASHEGVSSAK- 56	57 ----BRNTTVGVGLKQNWGSATNSNSPNDVPTVSNYSFKYENNPFLFGAGAGYSDG 112
Qy 115 PRILEAAAYQQENPKNTDNNDTNGKYYKHEALSRKDAMB---DQQTQVVLKNDGIFTMS 170	116 PRILEAAAYQQENPKNTDNNDTNGKYYKHEALSRKDAMB---DQQTQVVLKNDGIFTMS 170
Db 113 PRILEEVSTETFDVKQGNIN--YKNEAHRYCALSHNSADMSAANNNPVFLNEGLLDIS 170	113 PRILEEVSTETFDVKQGNIN--YKNEAHRYCALSHNSADMSAANNNPVFLNEGLLDIS 170
Qy 171 LMVNTCYDITTAEGVSFVPYACAGIADLITPKDNLKFAVQKGIGISYPITPEVSAFG 230	171 LMVNTCYDITTAEGVSFVPYACAGIADLITPKDNLKFAVQKGIGISYPITPEVSAFG 230
Db 171 FMLNACDVGVEGIPFSPYICAGITDLSMPBAPTNPKLSIQSKGLGYSISPEASVFIG 230	171 FMLNACDVGVEGIPFSPYICAGITDLSMPBAPTNPKLSIQSKGLGYSISPEASVFIG 230
Qy 231 GYHGVIGKNGKFEKIPVPTPVVNLDAPO-TTISASVTLDPYFGFGIG 275	231 GYHGVIGKNGKFEKIPVPTPVVNLDAPO-TTISASVTLDPYFGFGIG 275
Db 231 GHFKRIGNBFRDIPITIPTGSTLAKGNYPATVILDCHFGIEMG 276	231 GHFKRIGNBFRDIPITIPTGSTLAKGNYPATVILDCHFGIEMG 276

28k surface antigen 3 - *Ehrlichia chaffeensis*
 N: Alternate name: Map1
 C: Species: *Ehrlichia chaffeensis*
 C: Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
 C: Accession: JE0216
 R: Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
 Biochem. Biophys. Res. Commun. 247, 636-643, 1998
 A: Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe I
 A: Reference number: MUID:9821180; PMID:9647746
 A: Accession: JE0216
 A: Molecule type: DNA
 A: Residues: 1-280 <RED>
 A: Cross-references: UNIPROT:052106; GB:AF062761

Query Match 42.4%; Score 620; DB 2; Length 286;
 Best Local Similarity 47.3%; Pred. No. 5.1e-43;
 Matches 139; Conservative 42; Mismatches 89; Indels 24; Gaps 7;

Qy 1 MNYYKKILVRSLISLMSLTPYQSPADPVGSRNDNKEG-FYISAKKNPISIHKRKEAAE 59
 Db 1 MNCKKPFITTLTLMSPFGISLSPDV--QDNNISGNFYISGKMPMSASHGVFPAK 57

Qy 60 TPINGTNSITKVKYGLKKKGD----ITKKDDFTRVAPGIDFQNNLISGSGSIGYSD 113
 Db 58 ----ERNTVGVFGLIEQWDRCVTSRITLSDIFTVPPNFSKYBNLFSGAGAIGYSMD 112
 Qy 114 GPRIBLEAAYQQFNPKNTNNDDTNGEYKHFHALSKDAMEDO----QYVVLKNDGRT 167
 Db 113 GPRIBLEAAYQQFNPKNTNNDDTNGEYKHFHALSKDAMEDO----QYVVLKNDGRT 170

Qy 168 FMSLMLVNTQYDITAGVGSVTPYACAGIGADLITFKDNLNKFAYQKIGISPTIPVSA 227
 Db 171 DKSMLNACDVTSSEGIPSPVCAIGIDLVSNEAINKPKSYQKJLSPISPAASV 230

Qy 228 FIGGAYHGIGNKPEKIPVITPVVNLNDAPQ-TTSASVTLDVGFGGETGMRFTF 280
 Db 231 FIGGSHFKVIGNEFRDIPMIPSESAALGKGNPAAVTLDVFPYFGIELGGRFNF 284

RESULT 3
 JE0217
 28k surface antigen 4 - *Ehrlichia chaffeensis*
 N: Alternate name: Map1
 C: Species: *Ehrlichia chaffeensis*
 C: Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
 C: Accession: JE0217
 R: Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
 Biochem. Biophys. Res. Commun. 247, 636-643, 1998
 A: Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe I
 A: Reference number: MUID:9821180; PMID:9647746
 A: Accession: JE0217
 A: Molecule type: DNA
 A: Residues: 1-280 <RED>
 A: Cross-references: UNIPROT:052107; GB:AF062761

Query Match 41.2%; Score 603; DB 2; Length 280;
 Best Local Similarity 45.1%; Pred. No. 1.2e-41;
 Matches 133; Conservative 54; Mismatches 78; Indels 30; Gaps 10;

Qy 1 MNYYKKILVRSLISLMSLTPYQSPADPVGSRNDNKEG-FYISAKKNPISIHKRKEAAE 59
 Db 1 MNCKKPFITTLTLMSPFGISLSPDV--QDNNISGNFYISGKMPMSASHGVFPAK 57

Qy 60 TPINGTNSITKVKYGLKKKGD----ITKKDDFTRVAPGIDF--QNNLISGSGSIGYSD 113
 Db 58 ----ERNTVGVFGLKQWDGSTISKNSPENTPNVPSFYKVNPFGLFGAVGTLMN 112

Qy 114 GPRIBLEAAYQQFNPKNTNNDDTNGEYKHFHALSR----KDAMEDQYVVLKNDGITEM 169
 Db 113 GPRIBLEAAYQQFNPKNTNNDDTNGEYKHFHALSR----KDAMEDQYVVLKNDGITEM 170

Qy 170 SLAVNTCYDITAGVGSVTPYACAGIGADLITFKDNLNKFAYQKIGISPTIPVSAF 229
 Db 171 SLMLNACDVTSSEGIPSPVCAIGVGTLSNEAINKPKSYQKJLSPISPAASV 230

Qy 230 GGYHGIVGKNGKPEKIPVITPVVNLNDAPQTSAS---VTLDVGFGGETGMRFTF 280
 Db 231 GGFFHKVIGNEFRDIPMIPSESAALGKGNPAAVTLDVFPYFGIELGGRFNF 280

Query Match 39.9%; Score 583; DB 2; Length 278;
 Best Local Similarity 43.6%; Pred. No. 5.1e-40;
 Matches 126; Conservative 49; Mismatches 94; Indels 20; Gaps 7;

Qy 1 MNYYKKILVRSLISLMSLTPYQSPADPVGSRNDNKEG-FYISAKKNPISIHKRKEAAE 59
 Db 1 MNCKKPFITTLTLMSPFGISLSPDV--QDNNISGNFYISGKMPMSASHGVFPAK 57

Qy 60 TPINGTNSITKVKYGLKKKGD----ITKKDDFTRVAPGIDFQNNLISGSGSIGYSD 114
 Db 58 ----ERNTVGVFGLKQWDGSTISKNSPENTPNVPSFYKVNPFGLFGAVGTLMN 112

Qy 115 PRBLEAAYQQFNPKNTDNNDTNGEYKHFHALSRD--AMBDDQYVVLKNDGITEM 171
 Db 113 PRVEFEVSYETPDVKGQGNNYKNDA-HRYCLQGQDQDNNSGIPKTSVYLKSEGGLDISP 170

Qy 172 MNNTCYDITAGVGSVTPYACAGIGADLITFKDNLNKFAYQKIGISPTIPVSAF 231
 Db 171 MNACYDINNEISLPLSPVTCAGVGTLSNEAINKPKSYQKJLSPISPAASV 230

Qy 232 YYHGIVGKNGKPEKIPVITPVVNLNDAPQTSASVTLDVGFGGETGMRFTF 280
 Db 231 HFHKVIGNEFRDIPMIPSESAALGKGNPAAVTLDVFPYFGIELGGRFNF 278

RESULT 5
 I40882
 major antigenic protein - heartwater rickettsia
 C: Species: Cowdria ruminantium (heartwater rickettsia)
 C: Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C: Accession: I40882; S42827
 R: van Vliet, A.H.; Jongenel, F.; van Kleef, M.; van der Zeijst, B.A.
 Infect. Immun. 62, 1451-1456, 1994
 A: Title: Molecular cloning, sequence analysis, and expression of the gene encoding the in
 A: Reference number: I40882; PMID:94178956; PMID:8132352
 A: Accession: I40882
 A: Status: preliminary; translated from GB/EMBL/DB/DBJ
 A: Molecule type: DNA
 A: Residues: 1-284 <RES>
 A: Cross-references: UNIPROT:Q46327; EMBL:X74250; PIDN:CAA52309.1; PID:9454266
 C: Genetics:
 A: Gene: map1

Query Match 38.6%; Score 565; DB 2; Length 284;
 Best Local Similarity 43.1%; Pred. No. 1.5e-34; Gaps 6;
 Matches 129; Conservative 39; Mismatches 97; Indels 34; Gaps 6;

Qy 1 MNYYKKILVRSLISLMSLTPYQSPADPVGSRNDNKEG-FYISAKKNPISIHKRKEAAE 53
 Db 1 MNCKKPFITTLTLMSPFGISLSPDV--QDNNISGNFYISGKMPMSASHGVFPAK 52

Qy 54 KFSAEIPFPGTNSLTKVGLKKGDDITKDD----FTRVAPGIDFQNNLISGSGSIG 107
 Db 53 KNSIKEDSRD----TKAVFGKDKNDGKTPSGNTNSIIEKDYSFKYNNPFLGFGAGA 107

Qy 108 ICYXSMDDSPRIEELAAQCFQNPQNTDNDTNDGCBYXKHFALSRKDAEQQYVVLKNDGITEM 167
 Db 109 VGYSMGPRIEFVSTETDVNPQGGNYKNDAHMYCALDTASSTAGATTSVWNENLT 167

RESULT 4
 JE0216

Qy	168 FMSLMVNTCYDITAEGVSPVYACAGIGADLITIFKDLNLKFAYGKIGISYPTEVSA 227	Matches 96; Conservative 54; Mismatches 113; Indels 35; Gaps 9;
Db	168 DISMLNACAYDIMLDGMPSPVYACAGIGADLITIFKDLNLKFAYGKIGISYPTEVSA 227	Qy 1 MNYKKIL--VRSALISMSLILSPVQSPADP---VGSSTNDNKEGYTISAKN--PSI 49
Qy	228 FIGGYHGIGVGNKPEKIPVITPVVYLNDAPQTS----ASVTLDVGYGGBIGMRFETF 280	Db 1 MNYTRELFGGLSAAATVCACSLVSGAVVSPMSHEVASEGGVNGGSPVYGAASPAPSV 60
Db	228 FIGGHFHRTVIGNEFRDI--ATSKVETSSNASSAVSPGASAATLDVCHRGIBIGCRFVF 284	Qy 50 SHF--RKFAEETPINGTNSLTKVFLKKGDTIKDDFTRVAPGIDFQNLISGFSGS 107
RESULT 6		Qy 61 TSPDRMSEKETSYRGTDKSIATI-----DVSPANFSKSGCYTFAFSKLNLTFSFDA 113
JB0220	28k surface antigen 1 - <i>Ehrlichia canis</i>	Qy 61 TSPDRMSEKETSYRGTDKSIATI-----DVSPANFSKSGCYTFAFSKLNLTFSFDA 113
C;Species: <i>Ehrlichia canis</i>	C;Accession: JB0220	Qy 108 IGYSMDGPRIELAAVQQFNPKNTDDNNTDGEYKXH----FALSKDAMEDQOQYVVLK 162
C;Text: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004	C;Text: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004	Db 114 VGTSLGGARVELEASYRRE-----ATLADGQYAKSGAESLAAITDANITETNYFWVK 166
R;Reddy, G.R.; Sulsona, A.F.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.	R;Reddy, G.R.; Sulsona, A.F.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.	Qy 163 NDGTTFMSLMVNTCYDITAEGVSPVYACAGIGADLITIFKDLNLKFAYGKIGISYPIT 222
Biochem. Biophys. Res. Commun. 247, 636-643, 1998	Biochem. Biophys. Res. Commun. 247, 636-643, 1998	Db 167 IDENTNTSMNGGCDYVLEHTDLPVSPYCAIGRSFUDISKQVTTKLYRGKVGISYQFT 226
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe	A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe	Qy 223 PEVSAFIGGYHGIGVGNKPEKIPVITPVVYLNDAPQTSASAVTLDVGYGEGEIGHMRFETF 280
A;Reference: PMID:9647746	A;Reference: PMID:9647746	Db 227 PEISLVAGGFYHGLDESYKDIPAHNSVKFSG---EAKASVKAHADYGFNLGARPLF 281
A;Molecule type: DNA	A;Molecule type: DNA	
A;Residues: 1-287 <RED>	A;Cross-references: UNIPROT:Q9ZGJ0; GB:AF062762; PIDN: AAC26721.1; PID: g332	
RESULT 8		
Query Match 35.3%; Score 515.5; DB 2; Length 287;	JB0221 28k surface antigen 2 - <i>Ehrlichia canis</i>	
Best Local Similarity 39.3%; Pred. No. 1.7e-34; Mismatches 47; Indels 43; Gaps 7;	C;Species: <i>Ehrlichia canis</i>	
Matches 120; Conservative 47; Mismatches 95; Indels 43; Gaps 7;	C;Accession: JE0221	
Qy 1 MNYKKILVRSALISMSLILSPVQSPADPVSRTNDNKEGYTISAKNYPNTSHFRKFSAET 60	C;Text: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004	
Db 1 MKYKTPITPLVLTSPFHPIPYSPAASTIHN---EYISGRKMPATSHFGIFSAKE- 56	R;Reddy, G.R.; Sulsona, A.F.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.	
Qy 61 PINGTNSLTKVFLKKGDTIKDDFTRVAP---GIDFQNLISGSGTGYSMG 114	Biochem. Biophys. Res. Commun. 247, 636-643, 1998	
Db 57 ----EQSEPTKVLQDQLQRLSHNLTINNNDAKSLKVQNTSYKVNPFEGFAGALGYSIGN 112	A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe	
Qy 115 PRIBDAAYQQFNPKNTDDN-----DTDNEBYYKHFALSRKDAMED 155	A;Reference number: JB0221; MUID:98321180; PMID:9647746	
Db 113 SRIELEVSHBEIDTNPQGNRNLNDSHKCYCALSHGSHICSDGNSDWW-----TAKT 163	A;Molecule type: DNA	
Qy 156 QQYVVLKNDGITEWMSLMVNTCYDITAEGVSPVYACAGIGADLITIFKDLNLKFAYGKCI 215	A;Residues: 1-133 <RED>	
Db 164 DKFVLLKNSGGLDYSFMLNACYDTTKEPFSPTICAGITGDLISMFETQNKISYQRL 223	A;Cross-references: UNIPROT:085360; GB:AF062762; PIDN: AAC26722.1; PID: g332	
Qy 216 GISYPITPVYSAFVGGYHGIGVGNKPEKIPVITPVVYLNDAPQTSASAVTLDVGYGGIG 275	Query Match 15.6%; Score 227.5; DB 2; Length 133;	
Db 224 RINGTNSRVSFVAGHETKVGNEFKGPTLUDGSNTKQV-QSATVTLDVCHFGLIG 282	Best Local Similarity 41.4%; Pred. No. 1.6e-11; Mismatches 49; Indels 13; Gaps 4;	
Qy 276 MRFPT 280	Matches 58; Conservative 20; Mismatches 49; Indels 13; Gaps 4;	
Db 283 SRPFP 287	Qy 1 MNYKKILVRSALISMSLILSPVQSPADPVSRTNDNKEGYTISAKNYPNTSHFRKFSAET 60	
RESULT 9		
I39648 major surface protein 4 - Anaplasma marginale	Db 1 MNYTRELFGGLSAAATVCACSLVSGAVVSPMSHEVASEGGVNGGSPVYGAASPAPSV 60	
C;Species: Anaplasma marginale	Qy 61 PINGTNSLTKVFLKKGDTIKDDFTRVAPGIDFQNLISGSGTGYSMG 114	
C;Accession: I39648	Db 58 ---BKCKTIVVYGLKENWAGDAISQSPPDNFTIRNSFKYASNKFGLFAVAIGYSGS 113	
R;Oberle, S.M.; Barbet, A.F.	Qy 115 PRIBDAAYQQFNPKNTDDN 134	
Gene 136, 29-294, 1993	Db 114 PRIEVEMSYTAFDVKNQGNN 133	
A;Title: Derivation of the complete map4 gene sequence of Anaplasma marginale without c1		
A;Reference number: I39648; MUID:94124017; PMID:8294120		
A;Status: preliminary; translated from GB/EMBL/DBJ		
A;Molecule type: DNA		
A;Residues: 1-282 <RES>		
A;Cross-references: UNIPROT:Q07408; GB:L01987; PID: g142174; PIDN: AAC36877.1; PID: g142175		
C;Genetics:		
A;Gene: mspx4		
Query Match 26.4%; Score 386.5; DB 2; Length 282;		
Best Local Similarity 32.2%; Pred. No. 5.1e-24;		

A;Residues: 15-264 <RE2>	Db	148 LAHYKLSSN-----TIPVGGINETLDSKNNPAWAGAGIGAKY---AVTNIMID 194
A;Cross-references: EMBL:U07174; NID:9463910; PIDN: AAC13752.1; PID: g463913	Qy	255 A--PQTTSASVYTLDVGYFPGG 273
A;Accession: I69134	Db	195 ASYKXINACKVTSKHNHYGD 215
A;Status: translated from GB/EMBL/DDBJ		
A;Molecule type: DNA		
A;Residues: 18-264 <RE3>		
A;Cross-references: EMBL:U07174; NID:9463910; PIDN: AAC13753.1; PID: g463913		
Query Match 8.2t; Score 119.5; DB 2; Length 264;		RESULT 11
Best Local Similarity 23.0t; Pred. No. 0.25t; Mismatches 66; Indels 91; Gaps 14;		
Matches 59; Conservative 41; Mismatches 66; Indels 91; Gaps 14;		
Qy 5 KILVRSALISLMSILPVQSFADPVGSRTNDNGEFTYSAKVNFSIHSFRKSAETPING 64		S01892
Db 20 KVIAVSAL-AMAGMFSTQALAD----ESKTGPFYTGKAGASVMSL---ADQRLSG 67		hemolysin A precursor - <i>Vibrio cholerae</i> (strain Bl Tor 017)
Qy 65 TNSLTKVFKVGLKDGDTKQDDETRAVGFDIDFQNNLISLGFSGSIGYSD-----GPRI 117		N/Alternative names: Bl Tor hemolysin
Db 68 NGEBTTSKY---KGKD----GHD----TVFSGGIAAGYDFYQFSIPIVRT 105		C;Species: <i>Vibrio cholerae</i>
Qy 118 ELE-AYQQFNPNANTDNDTNGEYKHFALSRKDAMEDQQTIVLKNQGITMSLMLVNTC 176		C;Accession: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
Db 106 ELEFYARGKADSKVNVQDKDSWSSGYWR-----DD-----LXNE-VSYNTLMNAY 149		R;Alm, R.A.; Stroher, U.H.; Manning, P.A.
Qy 177 YDITAEGVSVFVYACAGIDLTIFKDNLK-----F 209		Mo.; Microbiol. 2, 481-488, 1988
Db 150 VDFRNDs-AFTPmVSAGIG----YAKEIHQKTGTGISTWDYGSSGREGSLSRSGSADNF 203		A;Title: Extracellular proteins of <i>Vibrio cholerae</i> : nucleotide sequence of the classical strain 569B.
Qy 210 AYQGKIGTSYPTPEVS 226		A;Reference number: S01892; MUID:89013889; PMID:3050359
Db 204 AWSLGAGYTRYDVTDPDIA 220		A;Accession number: S01892; MUID:89013889; PMID:3050359
Qy 28 VGSRTNDNPK-----EGFYS-----AKYNPISHFRKFSKAEETP-----61		A;Molecule type: DNA
Db 220 VGSATPDAKIVRISLDIDSTGAGHNDLGYRQFGASFTLDAYFREMSDIAQDIFRP 279		A;Cross-references: EMBL:Y00557
Qy 62 -INGTNSLTK--KVFGLKKDGTIKKDDFTRVAGIDFQNNLISGF-----SGSIGYSMGD 114		C;Genetics:
Db 280 VFNASNQKQILKTFPV---DN1NEK-----FRKEKEYSGFELGVTVGGVSGDG 325		A;Gene: hlyA
Qy 115 PRTLEAAVQQFNPKNTDNNDT-----NGEYGHFALSFRKDANEQDQVFLVRNGITF 169		C;Superfamily: Vibrio hemolysin A
Db 326 PKAKLEARRKLYQSRWLNTQDYRIERNAKNRLALHELSRTDRIATQ----SFD 380		F;1-18/Domain: signal sequence #status predicted <SIG>
Qy 170 SLMVNTYTDITAEGVSVFVPA-----CAGIGADLITTFDNLKFAYGOKGIG 216		F;19-738/Product: hemolysin A #status predicted <MAT>
Db 381 RCFVGEYTFDVKRISALTYASFPRMDVYKASATETSTDFLIDSSVIRPINGAYK 440		
Qy 217 ISYPITPEVSAPIGGYVHGIVGKPEKIPVITPVVLLNDAFQ---TTASVYTLD 266		
Db 441 HXYVGAQS-----YHG----FE-----DTPRRRTKSASTVTD 471		
A;Gene: STR0351		
RESULT 10		RESULT 12
AH0541		A27826
probable outer membrane adhesin STR0351 [imported] - <i>Salmonella enterica</i> subsp. <i>enterica</i>		A;Cross-references: UNIPROT:P08266; GB:X05709; GB:M29646; NID:95514651; PIDN:CAPI54
C;Species: <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i>		C;Species: <i>Drosophila melanogaster</i>
A;Note: this species has also been called <i>Salmonella typhi</i>		C;Date: 19-May-1989 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
Db 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002		C;Accession: A27826
Qy 30 SRNDNGEFTYSAKVNFSIHSFRKSAETPINGTNSA---TRKVFGLKQDGDIT 82		R;Falkenberg, D.; Dvoroniczak, B.; Faust, D.M.; Bautz, E.K.F.
Db 17 SATASAKEGYITKGAGTSVNVYGINSTPSQBEI-VNGHATLPDRYKGVFG---GGV- 70		J. Mol. Biol. 195, 155-162, 1991
Qy 83 KDDDFTRAVGFDQNNLISLGFSGSIGYSDGP-----RILEFAAYQOFNPKNTDNNDT 137		A;Title: RNA polymerase II of <i>Drosophila</i> . Relation of its 140,000 Mr subunit to
Db 71 -----AIGYDFYDFQFLPVRLEDTTFR-----GETD 97		A;Reference number: A27826; MUID:88011299; PMID:3116266
Qy 138 NGEYGHFALSFKD-AMEDQQVTVLKNQDITFMSLIVNTCDITAEVSVFVYACAGIG 195		A;Accession: A27826
Db 98 -----AKGGQDIIAFTGQPVHINVKNQ-VRMFTTYVNGYDF-HNISTATFPYISAGV 147		A;Molecule type: DNA
Qy 196 ADDITIFDNLKLFAYQCRKIGKQYPTPEVSAPIGGYVHGIVGKPEKIPVITPVVLLD 254		A;Residues: 54-1176 <FAL>
A;Status: preliminary		A;Cross-references: UNIPROT:P08266; GB:X05709; GB:M29646; NID:95514651; PIDN:CAPI54
A;Molecule type: DNA		R;Sitzler, S.; Oldenbourg, I.; Petersen, G.; Bautz, E.K.F.
A;Residues: 1-239 <PAR>		Gene 100, 155-162, 1991
A;Cross-references: GB:AL513382; PIDN: CAD08776.1; PID:g16501592; GSPDB:GN00176		A;Title: Analysis of the promoter region of the housekeeping gene DmRP140 by see
C;Genetics:		A;Reference number: PQ0154; MUID:91276237; PMID:1905256
A;Gene: STR0351		A;Accession: P00154